IN THE CLAIMS:

Please amend the claims as follows:

1. (Currently amended) A method of correcting oligo probe hybridization signals, the method comprising:

measuring signals from each oligo probe during multiple hybridizations within a linear range;

calculating a correction coefficient for each oligo probe by requiring **each oligo probe's**[[~~its~~]] signal average to be equal to a constant; and

correcting the signal for each oligo probe using the calculated correction coefficient**, wherein the corrected oligo probe hybridization signals are outputted to a computer memory**.

2. (Previously presented) The method of claim 1 comprising calculating an average and standard deviation for signals observed on each probe.

3. (Previously presented) The method of claim 2 comprising determining an uncertainty coefficient for each oligo probe.

4. (Original) The method of claim 3 wherein the uncertainty coefficient is based on a ratio of the average to the standard deviation.

5. (Previously presented) The method of claim 3 comprising deciding whether to redesign or disregard a probe having an uncertainty coefficient greater than a predetermined value.

6. (Original) The method of claim 5 wherein the predetermined value is approximately 1.0.

7. (Canceled).

8. (Currently amended) A method of obtaining correction coefficients for probes, the method comprising:

determining a dynamic range for gDNA binding;

measuring signals from each probe during multiple hybridizations with **the** gDNA within the linear range;

normalizing the signal intensities from **the multiple**~~different~~ hybridizations;

calculating an average signal for each probe from the normalized signal intensities; and

calculating a correction coefficient for each probe **by requiring the signal average to be equal to a constant**~~; and~~

~~calculating an uncertainty coefficient for each probe~~**, wherein the correction coefficients are outputted to a computer memory**.

9. (Original) The method of claim 8 and further comprising calculating an average and standard deviation for signals observed on each probe.

10. (Currently amended) The method of claim 9 **comprising determining an uncertainty coefficient for each oligo probe** ~~wherein the correction coefficients are calculated based on requiring its signal average to be equal to a constant~~.

11. (Original) The method of claim 10 wherein the uncertainty coefficient is based on a ratio of the average to the standard deviation.

12. (Currently amended) The method of claim **10**[[~~8~~]] and further comprising deciding whether to redesign or disregard a probe having an uncertainty coefficient greater than a predetermined value.

13. (Original) The method of claim 12 wherein the predetermined value is approximately 1.0.

14. (Cancelled)

15. (Withdrawn) A computer implemented method of using correction coefficients for oligo probes, the method comprising:

calculating a corrected signal for a probe using a corresponding correction coefficient;

calculating a weighting factor for a probe;

calculating an expression level for a gene as a function of the weighting factor; and

calculating an uncertainty of the gene expression.

16. (Withdrawn) The method of claim 15 and further comprising converting the corrected signal to a number of copies per cell.

17. (Withdrawn) The method of claim 16 and further comprising converting measurements of other genes to the number of copies per cell.

18. (Withdrawn) The method of claim 16 wherein the measurements of other genes are corrected based on a known number of copies per cell for a corrected signal.

19. (Withdrawn) The method of claim 15 wherein the weighting factor for a probe is proportional to an uncertainty coefficient associated with each probe.

20. (Withdrawn) The method of claim 19 wherein the weighting factor for a probe is equal to the uncertainty coefficient for the probe divided by the sum of uncertainty coefficients for all the probes for the gene.

21. (Withdrawn) The method of claim 15 wherein the expression level for a gene is the sum of weight times the corresponding corrected signal for the probes used to detect the gene divided by the number of probes used to detect the gene.

22. (Withdrawn) The method of claim 15 wherein the uncertainty of the gene expression level is based on the sum of the uncertainty coefficient for a probe times the corresponding corrected signal divided by the number of probes used to detect the gene.

23. (Withdrawn) The method of claim 15 wherein each probe has an associated uncertainty coefficient, and wherein the probe with the highest uncertainty is discarded prior to using the correction coefficients.

24. (Withdrawn) The method of claim 15 and further comprising making a call for the gene based on the uncertainty of the gene expression level.

25. (Withdrawn) The method of claim 24 wherein making a call further comprises:
subtracting a background from the average intensities of probes;
normalizing probe intensities globally;
applying the correction coefficient to each probe; and
determining a call based upon a Z-score for the gene.

26. (Withdrawn) The method of claim 24 wherein the call is made by a person.

27. (Withdrawn) A computer readable medium having instructions for causing a computer to perform a method of using correction coefficients for oligo probes, the method comprising:

calculating a corrected signal for a probe using a corresponding correction coefficient;

calculating a weighting factor for a probe;

calculating an expression level for a gene as a function of the weighting factor; and

calculating an uncertainty of the gene expression.

28. (Canceled).

29. (Previously presented) The method of claim 1, wherein the multiple hybridizations are with genomic DNA.

30. (Previously presented) The method of claim 3 comprising using the corrected signal to calculate an expression level for a gene by:

calculating a weighting factor for the oligo probe where if *m* (>=1) oligo probes are used to detect the expression level of the gene, w is the weighing factor, and *d* is the uncertainty coefficient, the weighting factor for the *i*th oligo probe can be calculated according to the formula: $w_i = \frac{d_i}{\sum_{l}^{m} d_l}$; and

using the calculated weighing factor to determine the expression value v according to the formula: $v = 1/m \sum_{i=1}^{m} w_i S_i^{corrected}$ where *m* is the number of the oligo probes used to detect the gene and $S_i^{corrected}$ is the calculated correction coefficient.